CRF Errors Corrected by th STIC System Branch

Serial Numb r: _09/899,634C_

CRF Processing Date: _01/10/03_
Edited by: _____
Verified by: _____ (STIC staff)

ENTERED

- ☐ Changed a file from non-ASCII to ASCII

- ☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.

- ☐ Edited a format error in the Current Application Data section, specifically: _____

- ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____.

- ☐ Added the mandatory heading and subheadings for "Current Application Data".

- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.

- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: _____

- ☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: _____

- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: _____

- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.

- ☐ Inserted colons after headings/subheadings. Headings edited included: _____

- ☐ Deleted extra, invalid, headings used by an applicant, specifically: _____

- ☑ Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☑ other invalid text, such as _"Unknown" in all Artificial/Unknown entries; "OTHER INFORMATION:" in Seq. 2_

- ☐ Inserted mandatory headings, specifically: _____

- ☐ Corrected an obvious error in the response, specifically: _____

- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.

- ☐ Corrected an error in the Number of Sequences field, specifically: _____

- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.

- ☐ Deleted *ending* stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____

- ☑ Other: _Inserted hard return in front of L2207 in Seq. 2_
  _____
  _____

*Examiner: The abov corrections must be communicated to th applicant in th first Office Action. DO NOT s nd a copy of this form.

3/1/95

OIPE

RAW SEQUENCE LISTING   DATE: 01/10/2003
PATENT APPLICATION: **US/09/899,634C** TIME: 10:01:43

Input Set : **A:\ptodc.txt**
Output Set: **N:\CRF4\01102003\I899634C.raw**

```
       3 <110> APPLICANT: Thomas Buhler; Reto Andreas Gadient; Reinhard Korn; Rao Movva
       5 <120> TITLE OF INVENTION: pCAR and its uses
       7 <130> FILE REFERENCE: 4-31499A
C-->   9 <140> CURRENT APPLICATION NUMBER: US/09/899,634C
C-->   9 <141> CURRENT FILING DATE: 2002-12-09
       9 <160> NUMBER OF SEQ ID NOS: 12
      11 <170> SOFTWARE: PatentIn version 3.1
      13 <210> SEQ ID NO: 1
      14 <211> LENGTH: 4286
      15 <212> TYPE: DNA
      16 <213> ORGANISM: Artificial
      18 <220> FEATURE:
      19 <221> NAME/KEY: CDS
      20 <222> LOCATION: (3229)..(4014)
      21 <223> OTHER INFORMATION: delta pCAR gene
      24 <400> SEQUENCE: 1
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      27 taagttgggt aacgccaggg ttttcccagt cacgacgttg taaaacgacg gccagtgcca       120
      29 agttgggatc tttgcattgg cccacggctc tcaggatggg gatgctcccc ttcagcaccc       180
      31 ggttcccctt ggaaactgat ggtcctggct ctgtggcatg gcagtggcac tgtgaggagc       240
      33 ccctaccagc agcacacagt gggtttggca ctgccacgct ccggatgccg cgctctgatc       300
      35 caacccccata atcaaggaa cccgaattgc cccatcattg cccccaccac ccccatcctg       360
      37 ccgggccctc acaccccacg ctgccttgtg gtgacattcc cagcccaaa cccacggctt       420
      39 catggctacc gcggggcatt tcccattgcc gccccattat cagctctgca cacctcccgc       480
      41 tgtacccatg cctcgtggct gcccttcttt gacgtataat cttctaatta atacccggcc       540
      43 ttgtcaaagt ggagcacaaa cgttaattaa ttccccagca ggcaggtaat taacagtgtg       600
      45 actccctttt tgctgcgagt ggggctgata cagagagatg tggcactatg gagcccacgg       660
      47 ggtcctggca ctgggtgccc acggaggtcc ccatgtgctg cagtgtcacc gcctccgagg       720
      49 tgacagtatt gtccctgcgg tgtccctgca gctcagctct gtccacaggg ccacctccag       780
      51 tttggagggg acacaatgca gccccgatgc aacccatcct cgcagcatcc cagggacaaa       840
      53 gaccccactg caagaccgca cacagggctg ggtcccgctc ccctaatatc tacagtgctt       900
      55 ttgcatggcc ccttaatcaa tgcagttaat cagcatgcgc tcatgcaccg ctctggagct       960
      57 gcaaagcccc tcgcagcgct gctcaccaac accgcgcacc gccccggccc agcctgcagc      1020
      59 acgcgctgca aacaggaaag aaacaaaata ttgcccaaat gtaggcaaag gcattcggct      1080
      61 gccttgacct ccgccgggcc gggccctgcc tgactcagct ccttactcag cgctcgcttc      1140
      63 ctccctccgg ctgccaccgc cgcagcgcac accctgacaa agagtggccc ttaacgggct      1200
      65 ctgaggtgca cccagcagtg cactcagcag tccaagggcc ggcctggagg tttgcaccgc      1260
      67 tacgtgctga cattagcatt gaacttggcc ctgggtagtg ctgcaggccg ggcggggtgg      1320
      69 gtgtagagag tgcagcgcgc gttgcacccg gtgccccttc ccctcccttg catcccagca      1380
      71 ggctgcaccc cagcaccagg cccgtgcatg catgctcctg gtgttattgc agcctggtgc      1440
      73 atgcatgcgt cttagtggtg cagcgctgtg catgcatcct ccttggtgtg tagcagctta      1500
      75 gtgcatgcat acccctcggt gttattgctg ctctgtgcac gcacgctcat tgtatcactt      1560
      77 catcccagtg catgcactca cactggagcg attgctgctc ggtgcacgca cactcattgt      1620
```

```
 79 atcacgtcag ctcagtggct gcacgcacac cggtgttatt gctgctcggt gcgtgcatgc  1680
 81 acatcagtgt cgctgcagct cagtgcatgc acgctcattg cccatcgcta tccctgcctc  1740
 83 tcctgctggc gctccccggg aggtgacttc aaggggaccg caggaccacc tcggggggtgg 1800
 85 ggggagggct gcacacgcgg accccgctcc ccctccccaa caaagcactg tggaatcaaa  1860
 87 aaggggggag gggggatgga ggggcgcgtc acacccccgc cccacaccct cacctcgagg  1920
 89 tgagccccac gttctgcttc actctcccca tctcccccccc ctccccaccc ccaattttgt 1980
 91 atttatttat tttttaatta ttttgtgcag cgatgggggc ggggggggg ggggcgcgcg   2040
 93 ccaggcgggg cggggcgggg cgaggggcgg ggcggggcga ggcggagagg tgcggcggca  2100
 95 gccaatcaga gcggcgcgct ccgaaagttt cctttatgg cgaggcggcg gcggcggcgg   2160
 97 ccctataaaa agcgaagcgc gcggcgggcg ggagtcgctg cgttgccttc gccccgtgcc  2220
 99 ccgctccgcg ccgcctcgcg ccgcccgccc cggctctgac tgaccgcgtt actcccacag  2280
101 gtgagcgggc gggacggccc ttctcctccg ggctgtaatt agcgcttggt ttaatgacgg  2340
103 ctcgtttctt ttctgtggct gcgtgaaagc cttaaagggc tccgggaggg ccctttgtgc  2400
105 gggggggagc ggctcggggg gtgcgtgcgt gtgtgtgtgc gtggggagcg ccgcgtgcgg  2460
107 cccgcgctgc ccggcggctg tgagcgctgc gggcgcggcg cggggctttg tgcgctccgc  2520
109 gtgtgcgcga ggggagcgcg gccggggggcg gtgccccgcg gtgcgggggg gctgcgaggg  2580
111 gaacaaaggc tgcgtgcggg gtgtgtgcgt ggggggggtga gcaggggggtg tgggcgcggc  2640
113 ggtcgggctg taaccccccc ctgcacccccc ctccccgagt tgctgagcac ggcccggctt  2700
115 cgggtgcggg gctccgtgcg gggcgtggcg cggggctcgc cgtgccgggc gggggggtggc 2760
117 ggcaggtggg ggtgccgggc ggggcggggc cgcctcgggc cggggagggc tcgggggagg  2820
119 ggcgcggcgg ccccggagcg ccggcggctg tcgaggcgcg gcgagccgca gccattgcct  2880
121 tttatggtaa tcgtgcgaga gggcgcaggg acttcctttg tcccaaatct ggcggagccg  2940
123 aaatctggga ggcgccgccg cacccccctct agcgggcgcg ggcgaagcgg tgcggcgccg  3000
125 gcaggaagga aatgggcggg gagggccttc gtgcgtcgcc gcgccgccgt ccccttctcc  3060
127 atctccagcc tcggggctgc cgcaggggga cggctgcctt cggggggggac ggggcagggc  3120
129 ggggttcggc ttctggcgtg tgaccggcgg ggtttatatc ttcccttctc tgttcctccg  3180
131 cagcccccaa gcttaaggtg cacggcccac gtggggacta gtgccacc atg gcg ctc    3237
132                                                        Met Ala Leu
133                                                         1
135 ctg ctg tgc ttc gtg ctc ctg tgc gga gtc gcg gat ctc acc aga agt     3285
136 Leu Leu Cys Phe Val Leu Leu Cys Gly Val Ala Asp Leu Thr Arg Ser
137     5                      10                    15
139 ttg agt atc act act cct gaa cag atg att gaa aag gcc aaa ggg gaa     3333
140 Leu Ser Ile Thr Thr Pro Glu Gln Met Ile Glu Lys Ala Lys Gly Glu
141 20                      25                    30                  35
143 act gcc tat ttg cca tgc aga ttt acc ctg ggt cca gaa gac cag ggg     3381
144 Thr Ala Tyr Leu Pro Cys Arg Phe Thr Leu Gly Pro Glu Asp Gln Gly
145                 40                      45                    50  .
147 ccg ctg gac atc gag tgg ctg ctg tca cca gct gat aat cag aag gtg     3429
148 Pro Leu Asp Ile Glu Trp Leu Leu Ser Pro Ala Asp Asn Gln Lys Val
149                 55                      60                    65
151 gat caa gtg att att tta tat tct gga gac aaa att tat gac gac tac     3477
152 Asp Gln Val Ile Ile Leu Tyr Ser Gly Asp Lys Ile Tyr Asp Asp Tyr
153             70                      75                    80
155 tac caa gat ctg aaa gga cga gta cat ttt aca agt aat gat ctc aaa     3525
156 Tyr Gln Asp Leu Lys Gly Arg Val His Phe Thr Ser Asn Asp Leu Lys
157     85                      90                    95
159 tca ggt gat gca tca ata aat gta aca aat cta cag ttg tca gat att     3573
160 Ser Gly Asp Ala Ser Ile Asn Val Thr Asn Leu Gln Leu Ser Asp Ile
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RAW SEQUENCE LISTING   DATE: 01/10/2003
PATENT APPLICATION: US/09/899,634C   TIME: 10:01:43

Input Set : A:\ptodc.txt
Output Set: N:\CRF4\01102003\I899634C.raw

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161 100                  105                  110                  115
163 ggc aca tat cag tgc aaa gtg aaa aag gct cct ggt gtt gga aat aag      3621
164 Gly Thr Tyr Gln Cys Lys Val Lys Lys Ala Pro Gly Val Gly Asn Lys
165                  120                  125                  130
167 aag att cag ctg aca gtt ctt ctt aag cct tca ggt aca aga tgt tat      3669
168 Lys Ile Gln Leu Thr Val Leu Leu Lys Pro Ser Gly Thr Arg Cys Tyr
169                  135                  140                  145
171 gtt gat gga tca gaa gaa att gga aat gac ttt aaa cta aaa tgt gaa      3717
172 Val Asp Gly Ser Glu Glu Ile Gly Asn Asp Phe Lys Leu Lys Cys Glu
173          150                  155                  160
175 cca aaa gaa ggt tca ctc cca tta cta tat gaa tgg cag aaa ttg tcc      3765
176 Pro Lys Glu Gly Ser Leu Pro Leu Leu Tyr Glu Trp Gln Lys Leu Ser
177      165                  170                  175
179 aat tca cag aag ctg ccc acc ttg tgg tta gca gaa atg act tca cct      3813
180 Asn Ser Gln Lys Leu Pro Thr Leu Trp Leu Ala Glu Met Thr Ser Pro
181 180                  185                  190                  195
183 gtt ata tct gta aaa aat gcc tct act gaa tac tct ggg aca tac agc      3861
184 Val Ile Ser Val Lys Asn Ala Ser Thr Glu Tyr Ser Gly Thr Tyr Ser
185                  200                  205                  210
187 tgt acc gtg aaa aac aga gtg ggc tct gat cag tgc ctg ctt cgc ctg      3909
188 Cys Thr Val Lys Asn Arg Val Gly Ser Asp Gln Cys Leu Leu Arg Leu
189          215                  220                  225
191 gat gtg gtt cct cct tca aat aga gct gga aca att gca gga gct gtt      3957
192 Asp Val Val Pro Pro Ser Asn Arg Ala Gly Thr Ile Ala Gly Ala Val
193          230                  235                  240
195 ata gga gtt ttg ctt gct cta gtg ctc att ggt ctt atc atc ttt tgc      4005
196 Ile Gly Val Leu Leu Ala Leu Val Leu Ile Gly Leu Ile Ile Phe Cys
197      245                  250                  255
199 tgt cgt taa tctagataag taatgatcat aatcagccat atcacatctg            4054
200 Cys Arg
201 260
203 tagaggtttt acttgcttta aaaaacctcc cacacctccc cctgaacctg aaacataaaa    4114
205 tgaatgcaat tgttgttgtt aacttgttta ttgcagctta taatggttac aaataaagca    4174
207 atagcatcac aaatttcaca aataaagcat tttttttcact gcattctagt tgtggtttgt   4234
209 ccaaactcat caatgtatct tatcatgtct ggatccccgg gtaccgagct cg            4286
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212 <210> SEQ ID NO: 2
213 <211> LENGTH: 261
214 <212> TYPE: PRT
215 <213> ORGANISM: Artificial
217 <220> FEATURE:
218 <223> OTHER INFORMATION: delta porcine CAR
220 <400> SEQUENCE: 2

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222 Met Ala Leu Leu Leu Cys Phe Val Leu Leu Cys Gly Val Ala Asp Leu
223 1              5                  10                  15
226 Thr Arg Ser Leu Ser Ile Thr Thr Pro Glu Gln Met Ile Glu Lys Ala
227          20                  25                  30
230 Lys Gly Glu Thr Ala Tyr Leu Pro Cys Arg Phe Thr Leu Gly Pro Glu
231          35                  40                  45
234 Asp Gln Gly Pro Leu Asp Ile Glu Trp Leu Leu Ser Pro Ala Asp Asn
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RAW SEQUENCE LISTING   DATE: 01/10/2003
PATENT APPLICATION: **US/09/899,634C**   TIME: 10:01:43

Input Set : **A:\ptodc.txt**
Output Set: **N:\CRF4\01102003\I899634C.raw**

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235      50                    55                    60
238 Gln Lys Val Asp Gln Val Ile Ile Leu Tyr Ser Gly Asp Lys Ile Tyr
239 65                    70                    75                    80
242 Asp Asp Tyr Tyr Gln Asp Leu Lys Gly Arg Val His Phe Thr Ser Asn
243                   85                    90                    95
246 Asp Leu Lys Ser Gly Asp Ala Ser Ile Asn Val Thr Asn Leu Gln Leu
247             100                   105                   110
250 Ser Asp Ile Gly Thr Tyr Gln Cys Lys Val Lys Lys Ala Pro Gly Val
251           115                   120                   125
254 Gly Asn Lys Lys Ile Gln Leu Thr Val Leu Leu Lys Pro Ser Gly Thr
255       130                   135                   140
258 Arg Cys Tyr Val Asp Gly Ser Glu Glu Ile Gly Asn Asp Phe Lys Leu
259 145                   150                   155                   160
262 Lys Cys Glu Pro Lys Glu Gly Ser Leu Pro Leu Leu Tyr Glu Trp Gln
263                   165                   170                   175
266 Lys Leu Ser Asn Ser Gln Lys Leu Pro Thr Leu Trp Leu Ala Glu Met
267             180                   185                   190
270 Thr Ser Pro Val Ile Ser Val Lys Asn Ala Ser Thr Glu Tyr Ser Gly
271           195                   200                   205
274 Thr Tyr Ser Cys Thr Val Lys Asn Arg Val Gly Ser Asp Gln Cys Leu
275       210                   215                   220
278 Leu Arg Leu Asp Val Val Pro Pro Ser Asn Arg Ala Gly Thr Ile Ala
279 225                   230                   235                   240
282 Gly Ala Val Ile Gly Val Leu Leu Ala Leu Val Leu Ile Gly Leu Ile
283             245                   250                   255
286 Ile Phe Cys Cys Arg
287             260
290 <210> SEQ ID NO: 3
291 <211> LENGTH: 1098
292 <212> TYPE: DNA
293 <213> ORGANISM: Artificial
295 <220> FEATURE:
296 <221> NAME/KEY: CDS
297 <222> LOCATION: (1)..(1098)
298 <223> OTHER INFORMATION: full length porcine CAR
301 <400> SEQUENCE: 3
302 atg gcg ctc ctg ctg tgc ttc gtg ctc ctg tgc gga gtc gcg gat ctc        48
303 Met Ala Leu Leu Leu Cys Phe Val Leu Leu Cys Gly Val Ala Asp Leu
304 1               5                   10                  15
306 acc aga agt ttg agt atc act act cct gaa cag atg att gaa aag gcc        96
307 Thr Arg Ser Leu Ser Ile Thr Thr Pro Glu Gln Met Ile Glu Lys Ala
308             20                  25                  30
310 aaa ggg gaa act gcc tat ttg cca tgc aga ttt acc ctg ggt cca gaa       144
311 Lys Gly Glu Thr Ala Tyr Leu Pro Cys Arg Phe Thr Leu Gly Pro Glu
312           35                  40                  45
314 gac cag ggg ccg ctg gac atc gag tgg ctg ctg tca cca gct gat aat       192
315 Asp Gln Gly Pro Leu Asp Ile Glu Trp Leu Leu Ser Pro Ala Asp Asn
316       50                  55                  60
318 cag aag gtg gat caa gtg att att tta tat tct gga gac aaa att tat       240
```

```
319 Gln Lys Val Asp Gln Val Ile Ile Leu Tyr Ser Gly Asp Lys Ile Tyr
320 65              70              75              80
322 gac gac tac tac caa gat ctg aaa gga cga gta cat ttt aca agt aat     288
323 Asp Asp Tyr Tyr Gln Asp Leu Lys Gly Arg Val His Phe Thr Ser Asn
324             85              90              95
326 gat ctc aaa tca ggt gat gca tca ata aat gta aca aat cta cag ttg     336
327 Asp Leu Lys Ser Gly Asp Ala Ser Ile Asn Val Thr Asn Leu Gln Leu
328             100             105             110
330 tca gat att ggc aca tat cag tgc aaa gtg aaa aag gct cct ggt gtt     384
331 Ser Asp Ile Gly Thr Tyr Gln Cys Lys Val Lys Lys Ala Pro Gly Val
332             115             120             125
334 gga aat aag aag att cag ctg aca gtt ctt ctt aag cct tca ggt aca     432
335 Gly Asn Lys Lys Ile Gln Leu Thr Val Leu Leu Lys Pro Ser Gly Thr
336         130             135             140
338 aga tgt tat gtt gat gga tca gaa gaa att gga aat gac ttt aaa cta     480
339 Arg Cys Tyr Val Asp Gly Ser Glu Glu Ile Gly Asn Asp Phe Lys Leu
340 145             150             155             160
342 aaa tgt gaa cca aaa gaa ggt tca ctc cca tta cta tat gaa tgg cag     528
343 Lys Cys Glu Pro Lys Glu Gly Ser Leu Pro Leu Leu Tyr Glu Trp Gln
344             165             170             175
346 aaa ttg tcc aat tca cag aag ctg ccc acc ttg tgg tta gca gaa atg     576
347 Lys Leu Ser Asn Ser Gln Lys Leu Pro Thr Leu Trp Leu Ala Glu Met
348             180             185             190
350 act tca cct gtt ata tct gta aaa aat gcc tct act gaa tac tct ggg     624
351 Thr Ser Pro Val Ile Ser Val Lys Asn Ala Ser Thr Glu Tyr Ser Gly
352             195             200             205
354 aca tac agc tgt acc gtg aaa aac aga gtg ggc tct gat cag tgc ctg     672
355 Thr Tyr Ser Cys Thr Val Lys Asn Arg Val Gly Ser Asp Gln Cys Leu
356         210             215             220
358 ctt cgc ctg gat gtg gtt cct cct tca aat aga gct gga aca att gca     720
359 Leu Arg Leu Asp Val Val Pro Pro Ser Asn Arg Ala Gly Thr Ile Ala
360 225             230             235             240
362 gga gct gtt ata gga gtt ttg ctt gct cta gtg ctc att ggt ctt att     768
363 Gly Ala Val Ile Gly Val Leu Leu Ala Leu Val Leu Ile Gly Leu Ile
364             245             250             255
366 gtg ttt tgc tgt cat aaa aag cgc aga gaa gaa aaa tac gaa aaa gaa     816
367 Val Phe Cys Cys His Lys Lys Arg Arg Glu Glu Lys Tyr Glu Lys Glu
368             260             265             270
370 gtg cat cat gat atc agg gaa gac gtg cct cct ccg aag agc aga acg     864
371 Val His His Asp Ile Arg Glu Asp Val Pro Pro Pro Lys Ser Arg Thr
372         275             280             285
374 tcc act gcc aga agc tac ctc ggc agc aac cac tcg tcc ctg gga tcc     912
375 Ser Thr Ala Arg Ser Tyr Leu Gly Ser Asn His Ser Ser Leu Gly Ser
376         290             295             300
378 atg tct cct tcc aac atg gaa ggc tat tcc aag act cag tat aac cag     960
379 Met Ser Pro Ser Asn Met Glu Gly Tyr Ser Lys Thr Gln Tyr Asn Gln
380 305             310             315             320
382 gta cca agc gaa gac ttt gaa cgc gct cct cag agt cca act ctc ccg     1008
383 Val Pro Ser Glu Asp Phe Glu Arg Ala Pro Gln Ser Pro Thr Leu Pro
```

RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 01/10/2003
PATENT APPLICATION: **US/09/899,634C**   TIME: 10:01:44

Input Set : **A:\ptodc.txt**
Output Set: **N:\CRF4\01102003\I899634C.raw**

<u>Invalid <213> Response:</u>
Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:1,2,3,4,5,6,7,8,9,10,11,12

VERIFICATION SUMMARY   DATE: 01/10/2003
PATENT APPLICATION: **US/09/899,634C**   TIME: 10:01:44

Input Set : **A:\ptodc.txt**
Output Set: **N:\CRF4\01102003\I899634C.raw**

L:9 M:270 C: Current Application Number differs, Replaced Current Application No
L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:399 M:283 W: Missing Blank Line separator, <220> field identifier

09899634

RAW SEQUENCE LISTING   DATE: 12/31/2002
PATENT APPLICATION: **US/09/899,634C**   TIME: 13:42:27

Input Set : **A:\20010608 pCAR and its uses seq 1 to seq id 12.ST25.txt**
Output Set: **N:\CRF4\12312002\I899634C.raw**

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   3 <110> APPLICANT: Thomas Buhler; Reto Andreas Gadient; Reinhard Korn; Rao Movva
   5 <120> TITLE OF INVENTION: pCAR and its uses
   7 <130> FILE REFERENCE: 4-31499A
C--> 9 <140> CURRENT APPLICATION NUMBER: US/09/899,634C
C--> 9 <141> CURRENT FILING DATE: 2002-12-09
   9 <160> NUMBER OF SEQ ID NOS: 12
  11 <170> SOFTWARE: PatentIn version 3.1
```

ERRORED SEQUENCES

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 212 <210> SEQ ID NO: 2
 213 <211> LENGTH: 261
 214 <212> TYPE: PRT
C--> 215 <213> ORGANISM: Artificial/Unknown 220> FEATURE:
W--> 216 <220> FEATURE:
 216 <223> OTHER INFORMATION: OTHER INFORMATION: delta porcine CAR
E--> 218 <400> SEQUENCE: 2
 220 Met Ala Leu Leu Leu Cys Phe Val Leu Leu Cys Gly Val Ala Asp Leu
 221 1               5                  10                  15
 224 Thr Arg Ser Leu Ser Ile Thr Thr Pro Glu Gln Met Ile Glu Lys Ala
 225              20                  25                  30
 228 Lys Gly Glu Thr Ala Tyr Leu Pro Cys Arg Phe Thr Leu Gly Pro Glu
 229          35                  40                  45
 232 Asp Gln Gly Pro Leu Asp Ile Glu Trp Leu Leu Ser Pro Ala Asp Asn
 233      50                  55                  60
 236 Gln Lys Val Asp Gln Val Ile Ile Leu Tyr Ser Gly Asp Lys Ile Tyr
 237 65                  70                  75                  80
 240 Asp Asp Tyr Tyr Gln Asp Leu Lys Gly Arg Val His Phe Thr Ser Asn
 241              85                  90                  95
 244 Asp Leu Lys Ser Gly Asp Ala Ser Ile Asn Val Thr Asn Leu Gln Leu
 245             100                 105                 110
 248 Ser Asp Ile Gly Thr Tyr Gln Cys Lys Val Lys Lys Ala Pro Gly Val
 249         115                 120                 125
 252 Gly Asn Lys Lys Ile Gln Leu Thr Val Leu Leu Lys Pro Ser Gly Thr
 253         130                 135                 140
 256 Arg Cys Tyr Val Asp Gly Ser Glu Glu Ile Gly Asn Asp Phe Lys Leu
 257 145                 150                 155                 160
 260 Lys Cys Glu Pro Lys Glu Gly Ser Leu Pro Leu Leu Tyr Glu Trp Gln
 261             165                 170                 175
 264 Lys Leu Ser Asn Ser Gln Lys Leu Pro Thr Leu Trp Leu Ala Glu Met
 265             180                 185                 190
 268 Thr Ser Pro Val Ile Ser Val Lys Asn Ala Ser Thr Glu Tyr Ser Gly
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RAW SEQUENCE LISTING   DATE: 12/31/2002
PATENT APPLICATION: **US/09/899,634C**   TIME: 13:42:27

Input Set : **A:\20010608 pCAR and its uses seq 1 to seq id 12.ST25.txt**
Output Set: **N:\CRF4\12312002\I899634C.raw**

```
269          195                  200                   205
272 Thr Tyr Ser Cys Thr Val Lys Asn Arg Val Gly Ser Asp Gln Cys Leu
273     210                  215                   220
276 Leu Arg Leu Asp Val Val Pro Pro Ser Asn Arg Ala Gly Thr Ile Ala
277 225                  230                   235                   240
280 Gly Ala Val Ile Gly Val Leu Leu Ala Leu Val Leu Ile Gly Leu Ile
281                  245                   250                   255
284 Ile Phe Cys Cys Arg
285              260
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RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 12/31/2002
PATENT APPLICATION: **US/09/899,634C**   TIME: 13:42:28

Input Set : **A:\20010608 pCAR and its uses seq 1 to seq id 12.ST25.txt**
Output Set: **N:\CRF4\12312002\I899634C.raw**

<u>Invalid <213> Response:</u>
Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:5,6,7,8,9,10,11,12

VERIFICATION SUMMARY　　　　　　　　DATE: 12/31/2002
PATENT APPLICATION:　**US/09/899,634C**　　TIME: 13:42:28

Input Set : **A:\20010608 pCAR and its uses seq 1 to seq id 12.ST25.txt**
Output Set: **N:\CRF4\12312002\I899634C.raw**

```
L:9 M:270 C: Current Application Number differs, Replaced Current Application No
L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:16 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:1
L:215 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:2
L:216 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:2
L:218 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:2
L:291 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:3
L:396 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:4
L:397 M:283 W: Missing Blank Line separator, <220> field identifier
L:397 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
```